em\_esthum19:\*
em\_esthum20:\*
em\_esthum21:\*

em\_esthum14:\* em\_esthum15:\*

em\_esthum16:\*

em\_esthum17: em\_esthum18:

em\_esthum10:\*
em\_esthum11:\*
em\_esthum12:\*
em\_esthum13:\*

em\_esthum22:\*
em\_esthum23:\*
em\_esthum24:\*
em\_esthum25:\*
em\_esthum26:\*

em\_estings: em\_esting:\* em\_esting:\* em\_esting:\* em\_esting:\* em\_esting:\*

em\_estom1:\*
em\_estom2:\*
em\_estov1:\*

em\_estov2: em\_estpl1: em\_estpl2: em\_estpl3: em\_estpl4: em\_estpl5: em\_estpl5: em\_estpl7:\* em\_estpl9:\*
em\_estpl10:\*
em\_estro1:\*
em\_estro2:\*

em\_estpl8:\*

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August 30, 2001, 20:37:17; Search time 1583.92 Seconds (without alignments) 3735.975 Million cell updates/sec
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1 agcgccttttgctggagggc......ggaagggaagggatcactt 626
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                 10228115 seqs, 4726426750 residues
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                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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em\_estrol3:\*
em\_estrol4:\*
em\_estrol5:\*
em\_estrol7:\*
em\_estrol9:\*
em\_estrol0:\*
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ep\_est25:\*
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gb\_est41:\*
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gb\_est44:\*

em\_estro10:\*
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em\_estro5:\*
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em\_estro7:\*
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em\_estro4:\*

9b_est18: 9b_est10: 9b_est11: 9b_est11: 9b_est15: 9b_est15: 9b_est15: 9b_est15: 9b_est15: 9b_est16:	900 est665 ** 900 est665 ** 900 est665 ** 900 est775 ** 900 est776 ** 900 est777 ** 900 est8177 ** 900 est88 ** 900 est89 ** 900 est88	9b_est103:* 9b_est104:* 9b_est106:* 9b_est106:* 9b_est106:* 9b_est66:* 9b_est69:* 9b_est70:* 9b_est71:* 9b_est73:* 9b_est93:*	stro23 stro23 stro23 stro23 stro7: st109:
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9b\_est110:\*
9b\_btc::
9b\_cst111:\*
9b\_btc::
em\_gss\_hum1:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.

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Email: cgapbs-rémail.nih.gov Tissue Procurement: DCTD/DTP CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.	Cunne distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Liki at:  http://image.linl.gov m column: 17 Plate: LiAM10302 row: m column: 17 High quality sequence stop: 661.  Location/Qualifiers  source //Organism="Homo sapiens" //Clone="ImAGE:4476088" //Clone="ImAGE:4476088" //Clone="ImAGE:4476088" //Clone="ImAGE:4476088" //Lissue_Lipe="NaHAGE:4476088" //Lissue_Lipe="ImAGE:4476088" //Lisue_Lipe="ImAGE:4476088" //Lisue_Lipe="ImAGE:4476088" /	Duery Match Best Local Similarity 100.08 Matches 321; Conservative 111 ggctgcagcggggtgagcgggc 111 ggctgcagcggggtgagcgggcggggggggggggggggg	NATIONALE PREFERENCE TO GENERAL STANDARD SATIONAL STANDARD STANDAR
Description	BG225521 60236/671 BF238010 601811713 BG337806 602435709 AI991236 wud1c09.x BE909218 601501478 BE906296 60150291 AI146858 qG68910.x H16108 y128a06.r1 BE56024 601500461 AI346818 qp58165.x H16108 y128a06.r1 BE56024 601346055 AV66406 AA442018 xx56600.x AW479270 24213 MAR BF733124 601788014 AA036192 m175612.r	AMASSAGA TATASAGA TAT	ALIGNMENTS  mRNA EST 13-FEB-2001 91 Homo sapiens CDNA clone IMAGE:4476088 5', 259  Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae, Homo. ci.nih.gov/. of Health, Mammalian Gene Collection (MGC) usberg, Ph.D.
SUMMARIES  Query Core Match Length DB ID	200.6 20	7.8.6 28.7 32.8 189 W13611 7.8.6 28.5 408 1 AA047994 7.8.6 28.5 408 1 AA047994 7.8.6 28.5 473 190 W78666 7.8.6 28.5 473 190 W78666 7.8.6 28.5 537 114 AW323711 7.8.6 28.5 744 150 BF533897 7.8.6 28.5 744 150 BF533897 7.8.6 28.5 744 150 BF533897 7.8.6 28.5 744 195 AK0186852 7.8.6 28.5 1105 192 AK0186852 7.7.4 28.3 349 4 AAA56479 7.7.4 28.3 349 191 W97090 1.7.7 28.3 384 191 W97090 1.7.7 28.3 384 191 W97090 1.7.7 28.3 384 191 W97090 66.8 27.1 918 144 BF100993 66.6 26.6 440 3 AA210183 1.6.8 26.0 668 173 BG08494 66.6 26.6 440 3 AA210183 1.6.8 26.0 144 BF0994315 1.8.6 25.3 309 141 BE860311	ALIGNMENTS  BG25521 744 bp mRNA EST 602367671F1 NIH_MGC_91 Homo sapiens CDNA clone RRNA sequence. BG25521 G1:12765259 BG25521.1 G1:12765259 FULDIAN HOMO sapiens

RESULT 1 BG25551 LOCUS DEFINITION

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Laxon:9606"
// Clone="IMAGE:453378"
// Clone="Liba" XH1-MXI-46"
// Lisue_type="lelomyosarcoma cell line"
// Lab_host="DH108 (phage-resistant)"
// Alab_host="DH108 (phage-resistant)
// Alab_host="D
                                                     In Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Parayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gow: b column: 03
High quality sequence stop: 710.
Location/Qualifiers
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   NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="fminary B-cells from tonsils (cell line)"
/lab host="DHIOB (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB); Site_1: XhOI;
Site_2: ECORI: CORA made by Oligo-dT priming.
Directionally cloned into ECORI/XhOI sites using the following 5, adaptor: GCORGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NHL_MOC'Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM895 row: i column: 04
High quality sequence stop: 670.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 748)
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BG337806 IG:13144342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 gccatcctggatgcgctggagaacctgaccgccgaggagctcaagaagttcaagctgaag 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 atggacgccttggacctcaccgacaagctggtcagcttctacctggagacctacggcgcc 354
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0
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/clone_lib="NIH_MGC_48"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.
E 1 (bases 1 to 687)
S NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Uppublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: egapbs.femail.nih.gov
Tissue Procurrement: Arroy
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
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/clone=lip="NIH_MGC_70"
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/lab_host="DH10B [phage-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE906296 888 bp mRNA EST 20-OCT-2000 601502291F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3904126 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 ggagccatgggggcgc-gcgcgacgccatcctggatgcgctggagaacctgacgccga 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GGAGCTCAAGAAGTTCAAGCTGAAGCTGTGTCGGTGCCGCTGCGCGAGGGCTACGGGCG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 687;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 270; DB 141;
Pred. No. 1e-44;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                             plate: LLAM9707 row: k column: 19
High quality sequence stop: 673.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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BE909218
BE909218.1 GI:10404770
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BE906296
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99.6%;
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                                                                                      Homo sapiens
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(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT773 vector. Library
went through one round of normalization. Tissue samples
provided by Dr. Brian Dieckgraefe (Washington University,
dieckelm.wustl.edu), colonic mucosa represents a range of
discase involvement from moderate to severe Crohn's
discase; samples include both perforating (fistulas) and
non-perforating samples. Library constructed by Bento
Soares and M. Fatima Bonaldo. "
194 c 197 g 135 t
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0
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/orsanism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:252608"
/clone="IMAGE:2525608"
/clone="IMAGE:252508"
/clone="IMAGE:252508"
/clone="IMAGE:252508"
                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 634)

NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
Insert Length: 708 Std Error: 0.00
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 atggggcgcgcgcgcgcgccatcctggatgcgctggagaacctgaccgccgaggagctc 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 43.2%; Score 270.4; DB 104; Length 634; Best Local Similarity 97.9%; Pred. No. 8.3e-45; Matches 274; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease"
/lab_host="DH10B (phage-resistant)"
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High quality sequence stop: 449.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
//organism="Homo sapiens"
//do xref="taxon:1966"
//clone="IND="1714818"
//clone=11b="Soares_placenta_8to9weeks_2NbHPBto9w"
//de_stage="two placentes: one from 8 weeks and another from 9 weeks post conception"
//lab_host="DH10B (ampicillin resistant)"
                                                         BE908204 675 bp mRNA EST 20-OCT-2000 601500461F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902319 5',
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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HH MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammallan Gene Collection (MGC)

Unpublished (1999)
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202 c 217 g
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                           Tumor Gene Index
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                                                                                                                              Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMG)09 row. e column: 23
High quality sequence stop: 659.
Flate: LLAMG: Sequence stop: 659.
Incation/Qualifiers
I.Corganism="Homo sapiens"
Alaxon:9606"
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamaila; Eutheria; Primates; Catarrhini; Hominidae; Homo.
11 (bases 1 to 888)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Entheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 678)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                       NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)
Unpublished (1999)
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41.4%; Soc
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Matches 259; Conservative 0;
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cDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Seq Clone distribution: NCI-CGAP clone distribution inficund through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 751 Std Error: 0.00
Seq primer: 400P from Gibco
High quality sequence stop: 457.
                                                                                                                                                                                                                                                                                                                        1..615
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1927233"
/clone=llb=NoI_cGAP_CO8"
/tissue_type="adenocarcinoma"
/lab_host="DH108"
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H16108.1 GI:880928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
   Tissue Procurement: ArC
   cDNA Library Preparation: Life Technologies, Inc.
   CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
   DNA Sequencing by: Incyte Genomics, Inc.
   CONSORTIUM/LINL at:
   CDNA Library Lib
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Emall: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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AI346818 1 GI:4084024
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illarity 100.0%; Pred. No. 4.1e-40;
Conservative 0; Mismatches 0;
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                    COMMENT
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/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by betto Scares and M. Fatima Bonaldo. "
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Sequencing Center
information can be
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 308)
Hillier, L., Cark, M., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Wailiamson, A., Wohldmann, P. and Wilson, R.

The WashU-Merck EST Project
Uppublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 gacgecatectggatgcgetggagaacetgaecgccgaggagetcaagaagttcaagetg 231
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yl28a06.rl Soares breast 3NbHBst Homo sapiens cDNA clone
IMAGE:159538 5', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1; Mammala; Eutheria; Primates; Catarrhin1; Hominidae; Homo.

1 (bases 1 to 262)

25 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Walliamson, A., Wohldmann, P. and Wilson, R.

The Washd-Merck EST Project
Unpublished (1995)

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Feax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Organismic Homo Saptens / Organismic Homo Saptens / Organismic Homo Saptens / Organismic Homo Saptens / Organismic Homo Saptens / Octone | Industria | Octone | Octo
                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
Seq primer: mob.REGA+Er
High quality sequence stop: 185.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 aagttcaagctgaagctgctgtcggtgccgctgcgcgagggctacggggcgatcccgcgg 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 ggagacctacggcgccgagctcaccgctaacgtgctgcgcgacatgggcctgcaggagat 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 ggcgcgcgcgacgcca-tcctggatgcgctggagaacctgaccgccgaggagctcaag 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 AAGTTCAAGCTGAAGCTGCTGTCGGTGCCCCTGCGC-AGGGCTACGGGCGCATCCCGCGG 120
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    /organism-"Homo sapiens"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                     Email: est@watson.wustl.edu
Insert Size: 868
High quality sequence stops: 209
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 868
Seq primer: MISRP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 ctgaagctgctgtcggtgccgctgcgagggctacggggcgcatcccgcgggggggcgctg 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               349 ggcgccgagctcaccgctaacgtgctgcgcgacatgggcctgcaggagatggccgggca 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W17108 262 bp mRNA EST 29-APR-1996 zb12d05.rl Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:301833 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares breast 3NbHBst"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"/db_xref="GDB:576463"
                                                                                                                                                                                                                                                                                                                                         Seg primer: M13kP1
High quality sequence stop: 209.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:159538"
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W17108.1 GI:1291525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 88.0 Matches 263; Conservative
                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Burkitt lymphoma"
//lab_host="DH10B (phage-resistant)"
//lab_host="DH10B (phage-resistant)"
//note="Organ: lymph; vector: porB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dr priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500pp for average
adaptor: size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
72 a 237 c 277 g 144 t
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                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 830)
                                                                                                                                                                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCNBS Fow: d column: 08
High quality sequence stop: 728.
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                                                                                                                                                                  NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 9e-35;
0; Mismatches 1; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:3678679"
/clone_lib="NIH_MGC_8"
                                 BE560228.1 GI:9803948
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Best Local Similarity 99.1%;
Matches 232; Conservative
                                                                                                                                                                                                          Unpublished (1999)
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sednence
                                                                                           Homo sapiens
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//Organism="Homo sapiens"
//Organism="Homo sapiens"
//Organism="Homo sapiens"
//Clone="Inace: 1867892s"
//Clone="Inace: 1867892s"
//Lissue_type="Burkitt lymphoma"
//Lissue_type="Burkitt lym
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
Clound through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM356 row: n column: 14
High quality sequences stop: 649.
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                                                                                                          NIH MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 2.1e-34;
0; Mismatches 44;
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84.8%;
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                                                                                                                                                                                                 Unpublished (1999)
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Matches 245; Conservative
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                                                                              REFERENCE
AUTHORS
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Contact: Wilson RX School of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Fax: 314 286 1810 Fax: 3185 Form Mersham Liny sequence stop: 385. Location/Qualifiers
 Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                              source
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ORIGIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 446)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Walie WashU-Merck EST Project 1997,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
Bovidae; Bovinae; Bos.
1 (bases 1 to 555)
Sugimoto,Y., Hirotsune,S., Takasuga,A., Itoh,R., Jitohzono,A. and
                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage_fetus
//deb_host="nulub"
//note="voctor: pZL1: Site_1: Sal1; Site_2: Not1; Poly A
was deleted from a Not1 site"
a 178 c 157 g 110 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA442U18 446 bp mRNA EST 02-JUN-1997 zw56c01.rl Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGES774048 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 ggatcctggagccatggggcgcgcgcgcgccatcctggatgcgctggagaacctgac 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 AGGGGGGGGGCCCAAAAAGTTCAAGATGAAGCTGCTTTCAGTGCCGCTGCGGGAAGGCTA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 egggegeatecegegggggggegetgetgtecatggaegeettggaecteacegaeaaget 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 TGGACGCATCCCCCGGGGGACCCTGCTCCCCTGGATGCCGTGGACCTCACCGACAACT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 GGACCCGGAGACATGGGGTGCACACGCGATGCCATCCTGGATGCGCTGGAGAACATGAC 74
                                                     Suzuki, H

Bovine (DNA sequencing

Unpublished (2000)

Contact: Yoshikazu Sugimoto

Animal Genetics Division

Shirakawa Institute of Animal Genetics

Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan

Fax: 81-248-25-5541
                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51; Indels
                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Bos taurus brain fetus"
/tissue_type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.9%; Score 218.4; DB 32;
83.0%; Pred. No. 2.3e-34;
Live 0; Mismatches 51;
                                                                                                                                                                                                                                                                                                                /organism="Bos taurus'
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                    /clone="ElbR040C01"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA442018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
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                                                                       TITLE
JOURNAL
                   REFERENCE
                                     AUTHORS
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AA442018
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                              FEATURES
                                                                                                             COMMENT
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66 CAGCGCCGGACGCCANTCCGTGNGGATGCGCTGGAGAACNCGTGACCGCCGAGGAGGTCA 125
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                                                                                                                                                                                                                                                                      108 ggcggctgcagcggggtgagcggcggcagcggccggggatcctggagccatgggggcgcg 167
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                               218 a-gaagttcaagctgaag-ctgctgtcggtgccgctgcgagggctacggggcatccc
                                                                                                                                                                                                                                                                                                                                                                              126 ACGAAGTTCAAGCTGAAGACTGCTGTCGGTGCCGCTGCGCGAGGGCTACGGGCGATCCC
                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                          34.2%; Score 214; DB 7; Length 446; 85.6%; Pred. No. 1.7e-33; Indels 1.ve 0; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  395 agatggccgggcagctgcaggcggccacgcacagggtgagccgccc 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: August 30, 2001, 22:09:02 Job time: 5505 sec
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Matches 298; Conservative
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Sequence Seq
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Patent No. 5876991
GENERAL INFORMATION.
APPLICANT: DeHOff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
US-08-873-970-97

US-09-158-75-97

US-09-158-767-7

US-09-158-767-1

US-08-439-009A-1

US-08-915-028-2

US-09-385-028-1

US-08-915-028-1

US-08-917-1

US-08-972-629-1

US-08-972-630-1

US-08-972-630-1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
COMPUTER: BENDEALIBLE
COMPUTER: BASIL(BOS) Text Only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION INFORMATION:
TELECOMMUTCATION INFORMATION INFORMAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
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20110..31284
      CDS
350..14002
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-804-227C-7
                                                                                                 August 30, 2001, 20:42:32; Search time 39:27 Seconds (without alignments) 3017.794 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                      US-09-691-763B-4
626
1 agcgccttttgctggagggc......ggaagggaagggatcactt 626
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Sequence 7,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_NA:*
1    /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2:    /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3:    /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4    /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5:    /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
6:    /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
                                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT US95 09323 - 1
US-08-459-586-15
US-08-282-696-4
US-08-282-696-4
US-08-788-662-4
US-09-036-9878-25
US-08-845-998-7
US-09-206-537-7
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PCT-US95-09323-10
US-08-476-519-1
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US-09-428-517-1
US-09-385-028-14
US-08-455-001-1
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US-09-385-028-1
US-07-751-891B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-997-080-97
US-08-997-362-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                            nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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11765
11899
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Match Length
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51.2
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48.4
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                                                                                                                                                                                                                       Run on:
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Result No.

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329 gottotacctggagacctacggcgccgagctcaccgctaacgtgctgcgcgacatgggcc 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                449 octocaccccgtcttcccctccacccaccagcgcttaccccgcgggctcttccgct 507
                                                                                                                                                                                                                              Score 52.6; DB 2; Length 44377;
Pred. No. 0.023;
0; Mismatches 79; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7.7, Application US/08042747A

Patent No. 5487969

GENERAL INFORMATION:
APPLICANT: Black, Darla
APPLICANT: Black, Darla
APPLICANT: Scinicariello, Franco
APPLICANT: Milliard, Julia K.
TITLE OF INVENTION: Cloning and Amplification of Monkey B
TITLE OF INVENTION: Virus Genes
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cox 6 Smith Incorporated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vergion #1.25
CURENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Cox & Smith Incorporated
112 East Pecan Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/ACENT INFORMATION:
NAME: Haymond, W. Bradley
REGISTRATION NUMBER: 35186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 210-254-5500
TELEFAX: 210-226-8395
                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.9%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2943 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                    CDS
31329..36071
                                                                                                                                   CDS . 36155..41830
           CDS
20110..31284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 210-226-8395
TELEX: 767609
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        San Antonio
Texas
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NAME/KEY: CDS
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      NAME/KEY:
LOCATION:
FEATURE:
                                                                  NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
                                                                                                                                                     ; LOCATION:
US-08-804-198-1
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US-08-042-747A-7
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                                                                                                                                                                                                                                                                                                                              DD 16843 GCATCGACCTCCCCACCTTCCAACACGCTGCTGGCTGGCCGCCCCTCCC 16902
                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 16963 CCGCCGCGCGGGAACTGCCCGGCACCGACACCGAGGTGTGGACCGGCCGCATATCCGCT 17021
                                                                                                                                                                                                                                                  329 gettetacetggagacetacggcgccgagetcaccgctaacgtgetgcggacatgggce 388
                                                                                                                                                                                                                                                                                                                                                                                                                    449 cetecaccogtettteccetecaccaaccaagcgettaccecgggggetettecget 507
                                                                                                                                                                    Query Match 8.4%; Score 52.6; DB 2; Length 44377; Best Local Similarity 55.9%; Pred. No. 0.023; Matches 100; Conservative 0; Mismatches 79; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Burgett, Stanley G.
APPLICANT: Burgett, Stuart A.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Rosteck, Paul R., Jr.
TILLE OF INVENTION: PLATENOLIDE SYNTHASE GENE NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELL 1138
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/40,198
FILING DATE:
CLASSIFICATION: 435
ATTORREY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REPERENCE/POCKET NUMBER: P9113
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION TORE SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 443377 Dasse pairs
TWORF. nucleic acid
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                                                                    CDS
36155..41830
        CDS
31329..36071
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nucleic acid
nernwess: single
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14046..20036
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LOCATION: 350..14002
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NAME/KEY:
LOCATION:
FEATURE:
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COUNTRY: U
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LOCATION:
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US-08-804-227C-7
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APPLICANT: Ryan, Michael J.
APPLICANT: Lotvin, Jason A.
APPLICANT: Strathy, Nancy
APPLICANT: Fanthin, Susan E.
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: clontetracycline and tetracyline Formation and cosmids
TITLE OF INVENTION: useful therein
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                                                                                                                                                                                                                  cocoggagoogacttootootggtoggotgcagoggggtgagoggcggcagoggccg 142
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                                                                                                                                                                         23 cggaccgggggcggggagtcgggagaccagagtgggaggaaggcggggagtccaggttccg 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                508 AGGCCACCATGTACTACAAGGACGTGACCGTCTCGCAGGTCGGGTTCGGCACCGGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 acgggcgcatcccgcgggggcgcgctgtccatggacgccttggacctcaccgacaagc
                                                                                                                              0;
                                                                                      Length 2943;
                                                                                 8.2%; Score 51.2; DB 1; Length 2 ilarity 44.5%; Pred. No. 0.038; Conservative 0; Mismatches 253; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA
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One Cyanamid Plaza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08125468
Patent No. 5589385
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ATTORNEY/AGENT INFORMATION:
NAME: TSEVDOS, ESTELLE J
REGISTRATION NUMBER: 31,145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
87..2744
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-08-125-468-1/c
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                                                                                 Query Match
Best Local Simi
Matches 203;
; LOCATION:
US-08-042-747A-7
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GENERAL INFORMATION:
APPLICANT: Ryan, Michael J.
APPLICANT: Lotvin, Jason A.
APPLICANT: Strathy, Nancy
APPLICANT: Strathy, Nancy
APPLICANT: Fantini, Susan E.
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: useful therein
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8.1%; Score 50.8; DB 1; Length 3
Best Local Similarity 45.6%; Pred. No. 0.051;
Matches 219; Conservative 0; Mismatches 257; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
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REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         One Cyanamid Plaza
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                        TELEFOX: (201)831-3305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CRRACTERISTICS:
LENGTH: 30001 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
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1579 gacgecegegageaccacaaccreaecresaaccagesegecaresreseceaecaecae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 aggiticogcocoggagoogacticotootggitoggoggotigoagogggiggigg 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 agcggccggggatcctgg··agccatggggcgcgcgcgcgacgccatcctggatgcgctg 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 gagaacctgaccgccgaggagctcaagaagttcaagctgaagctgctgtcggtgccgctg 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 cgcgagggctacggggcgcatcccgcgggggcgctgctgtccatggacgcttggacctc 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373 ctgcgcgacatgggcctgcaggagatggccgggcagctgcaggcggccacgcaccagggt 432
                                   Containing It and Methods of Using Isoamylases
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                                                            NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grace L. Bonner, Monsanto Company, BB4F
STREET: 700 Chesterfield Parkway No. 5750876th
                                                                                                                                                                                                                                                                                                                                       SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281902
FILING DATE: 28-JUL-1994
ATTORNEY/ARDIT INFORMATION:
NAME: Bonner, Grace L.
REGISTRATION NUMBER: 32,963
FERERGEOE/DOCKET NUMBER: 38,963
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-647
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,519
                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 2244 base pairs
nucleic acid
EDNESS: double
                                                                                                                                                                                                                                  ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                          STREET: /vc
CITY: St. Louis
                                      FITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
; LOCATION:
US-08-476-519-10
                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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Patent No. 5750876
Patent No. 5750876
Patent No. 5750876
Patent No. 5750876el Isoamylase Gene, Compositions
TITLE OF INVENTION: No. 5750876el Isoamylase Gene, Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.1%; Score 50.8; DB 2; Length 30001; Best Local Similarity 45.6%; Pred. No. 0.051; Matches 219; Conservative 0; Mismatches 257; Indels 4;
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,933
FILING DATE:
                                                                                                                                                                                                                                                                                                         NAME: Tsevdos, Estelle J
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,255-02
RELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3241
                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,468
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 30001 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-474-933-1
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MEDIUM TYPE: Floppy
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Missouri
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STATE:
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                                     1759 GCGCCCAACTGGCTGTACTGGAGCCGCAGCGCCTCGAGGCCCGACCACGAGCCTACACC 1818
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433 gageegeeceegtteecetecaceeegtettteecetecaacaacaacagegettaecee 492
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Containing It and Methods of Using Isoamylases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 8.0%; Score 50; DB 5; Length 2244; Local Similarity 44.9%; Pred. No. 0.064; es 230; Conservative 0; Mismatches 280; Indels
                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Novel Isoamylase Gene, Compositions TITLE OF INVENTION: Containing It and Methods of Using NUMBER OF SEQUENCES: 11
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
APPLICATION NUMBER: PCT/US95/09323
                                                                                                                    1819 AAGCGCCTGATCGCGTTCCGCAAGGCGCACCC 1850
                                                                              493 gegggetetteegetttetgtteeteetaece 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281902
FILING DATE: 28-JUL-1994
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                      Sequence 10, Application PC/TUS9509323 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2244 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION:
PCT-US95-09323-10
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Matches
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1492 ACGSTCACCCCGGCACCCTGGCCACGCGCTTCGCCGGCTCCAACGACCTGTACGGCGAC 1551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1432 GAGTGGAACGGCCTCTACCGCGACGCGCTGCGCAAGAAGCAGAACAAGCTCGGCGTGGAA 1491
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                                                                                                                                                                                                                                       Sequence 1, Application US/08476519
Sequence 1, Application US/08476519
Fatent No. 5750876
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: KISHOTE, Ganesh M.
APPLICANT: KISHOTE, Ganesh M.
APPLICANT: KISHOTE, Bradley M.
TITLE OF INVENTION: Containing It and Methods of Using Isoamylases NUMBER OF EXQUENCES: 11
CORRESPONDENCE: 11
ADDRESSEE: Grace L. Bonner, Monsanto Company, BB4F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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Pred. No. 0.064;
Wismatches 280; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: Grace L. Bonner, Monsanto Company, BB4F 700 Chesterfield Parkway No. 5750876th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 0S/08/476,519
                                                                                                                            1819 AAGCGCCTGATCGCGTTCCGCAAGGCGCACCC 1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bonner, Grace L.
REGISSPRATION NUMBER: 32,963
FEFERENCE/DOCKET NUMBER: 38-21(13577)A
TELECOMMUNICATION INFORMATION:
                                                                             493 gegggetetteegetttetgtteeteetaeee 524
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281902
FILING DATE: 28-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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US-08-476-519-1
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TELEFAX: (314)537-6047
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 44.9*
Matches 230; Conservative
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1612 AACGACCTGTACGCCTACAACGACAAGCAGAACAACCAGCCGTGGCCGTACGGGCCGTCC 1671

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                                      1612 AACGACCTGTACGCCTACAACCAAGCAGAACAACCAGCCGTGGCCGTACGGGCCGTCC 1671
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                                                                                                                        1672 GACGGCGGCGAGGACCACAACCTGAGCTGGAACCAGGGCGGCATCGTCGCCGAGCAGCGC 1731
                                                                                                                                                                                                         1732 AAGGCCGCGCGCACCGGACTGGCGTTGCTGATGCTCAGCGCCGGCGTGCCGATGATCACC 1791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 agoggoogggatcctgg--agocatggggogogogogogogocatcctggatgcgctg 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Novel Isoamylase Gene, Compositions
TITLE OF INVENTION: Containing It and Methods of Using Isoamylases
                                                                                253 cgcgagggctacggggcgcatcccgcgggggggggcgctgctgtccatggacgcttggacctc
                                                                                                                                                              313 accgacaagetggteagettetacetggagacetacggegeegggggeteacegetaaegtg
                                                                                                                                                                                                                                                                                   1792 GGCGGCGACGAGGCGCTGCGCACCCAGTTCGGCAACAACAACAACTACAACTGGATTCG
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0.064;
ches 280; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 11
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 50; DB 9
Pred. No. 0.064
0; Mismatches
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PRICING DATE:
CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/281902
FILLING DATE: 28-JUL-1994
; INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2334 base pairs
TYPE: __wecs: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application PC/TUS9509323 GENERAL INFORMATION:
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Best Local Similarity 44.9%;
Matches 230; Conservative (
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APPLICANT: Jones, Thomas R.
APPLICANT: Campbell, Ann E.
TITLE OF INVENTION: Identification of a Human
TITLE OF INVENTION: Cytomegalovirus Gene Region Involved in Down-Regulation of
TITLE OF INVENTION: MIC Class I Heavy Chain Expression
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                                                                                                                                                                                                                                                   1792 GGCGGCGACGAGGCGCTGCGCACCCAGTTCGGCAACAACAACAACATACAACCTGGATTCG 1851
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                                                                                                 313 accgacaagctggtcagcttctacctggagacctacggcgccgagctcaccgctaacgtg
                                                                                                                                                                                                373 ctgcgcgacatgggcctgcaggagatggccgggcagctgcaggcggccacgcaccagggt
gageegeecegtteceetecacecegtettteceetecaceceacaceagegettacece
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,586
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,425-01
TELECHONE: 201-683-2158
                                                                                                                                                                                                                                                                                                                                                                                                                                      1912 AAGGGCTGATGGGTTCGGAAGGGGGACCC 1943
                                                                                                                                                                                                                                                                                                                                                                                                     493 gegggetetteegetttetgtteeteetaece 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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United States
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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GENERAL INFORMATION:
APPLICANT: Jones, Thomas R.
APPLICANT: Campbell, Ann B.
TITLE OF INVENTION: Identification of a Human
TITLE OF INVENTION: Cytomegalovirus Gene Region Involved in Down-Regulation of
TITLE OF INVENTION: MHC Class I Heavy Chain Expression
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive
                                                                                                                                     83 ccccggagccgacttcctcctggtcggcggctgcagcggggtgagcggcggcggcggccg 142
                                                                                                                                                                                                                               143 gggatcctggagccatggggcgcgcgcgcgacgccatcctggatgcgctggagaacctga 202
                                                                                                                                                                                                                                                           203 ccgccgaggagctcaagaagttcaagctgaagctgctgtcggtgccgctgcgagggct 262
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     Gaps
                                                                                          104 CGTACGCCCCCCCCCCCCCCCCCCATTTCCCTCCTAACCCCGACGCCCACCCCGTGC 163
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                                                  cggaccgggggggggggggggagaccagagtgggaggaaggcgggggagtccaggttccg
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     Mismatches 231; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CNERBUT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,586
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02-JUN-1995
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; Patent No. 5720957
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TELEPRIONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 18994 base pairs
TYPE: nucleic acid
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     Matches 188; Conservative
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APPLICANT: Campbell, Ann E.
TITLE OF INVENTION: Identification of a Human
TITLE OF INVENTION: Cytomegalovirus Gene Region Involved in Down-Regulation of
TITLE OF INVENTION: MHC Class I Heavy Chain Expression
WUMBER OF SEQUENCES: 20
104 CGTACGGCGCCGCCGCGGGGGGGGGGGGTTTTGCGTGCCTAACGCGGACGCGCACGCGGTGG 163
                                                                                                                                  143 gggatcctggagccatggggcgcgcgcgcgcgccatcctggatgcgctggagaacctga 202
                                                                                                                                                                               224 CGGTCCGCCGCGCGTCGGGGACCGTGCCGCGCCCATGCTGGTGGTGCTGCTGGACGACC 283
                                                                                                                                                                                                                          203 ccgccgaggagctcaagaagttcaagctgaagctgctgtcggtgccgctgcgcgagggct 262
                                                                                                                                                                                                                                                                     284 TGGGCGCCGTGTTCGGGTACTGCCCGCTGGACGGCCACGTGTACCCGCTGGCGGCGGGGC 343
                                                                                                                                                                                                                                                                                                                                              323 tggtcagcttctacctggagacctacggcgccgagctcaccgctaacgtgctgcgcgaca 382
                                                                                                                                                                                                                                                                                                                                                                                                                                          383 tgggcctgcaggagatggccgggcagctgcaggcggccacgccacgggtgagccgcc 441
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                                                                                     164 TCGGGGCGGACGCGGCAGCAGCGGCGCCGACGGTGATGGTGGGTTCGACAGCGATGC
                                             7.9%; Score 49.4; DB 2; Length 1765; 44.9%; Pred. No. 0.083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New Jersey
COUNTRY: United States
ZIP: 07470-03426
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/08/282,696
FILING DATE: 29-JUL-1994
CLASSIFICANION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
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Patent No. 5846806
GENERAL INFORMATION:
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NAME: BETNATCH Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,42
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3246
TELEPHONE: 201-831-3305
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SEQUENCE CHARACTERISTICS:
LENGTH: 1765 base pairs
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EDNESS: single
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Length 18994;

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Db 14144 CGTACGCCCCCCCCCCGCCGGGGCGCGATTTGCGTGCCTAACGCGGACGCGCACGCGGTGG 14203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   383 tgggcctgcaggagatggccgggcagctgcaggcggccacgcaccagggtgagccgccc 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 acgggcgcatcccgcgggggggcgctgctgtccatggacgccttggacctcaccgacaagc
                                                                                                                                       7.9%; Score 49.4; DB 2; Length 1 44.9%; Pred. No. 0.092; Live 0; Mismatches 231; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08758662
Patent No. 6114150
GENERAL INFORMATION:
APPLICANT: Welssman, Sherman
APPLICANT: Baskaran, Namadev
ITILE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: SEED and BERRY LLP
STREET: 701 Fifth Avenue, 6300 Columbia Center
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: No. 6114150tenburg Ph.D., Carol
REGISTATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 390036.402C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/758,662
FILING DATE: 29-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
; STRANDEDNESS; single
TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-282-696-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (206) 622-4900 TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                       Query Match
Best Local Similarity 44.99
Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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US-08-758-662-4
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APPLICANT: Campbell, Ann E.
TITLE OF INVENTION: Identification of a Human
TITLE OF INVENTION: Cytomegalovirus Gene Region Involved in Down-Regulation of
TITLE OF INVENTION: MIC Class I Heavy Chain Expression
CORRESPONDENCES: 20
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                           Db 14144 ceracecececececeseseseseseses armiceracera ceraaceces acces a 14203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 gggatcctggagccatggggcgcgcgcgcgcgcatcctggatgcgctggagaacctga 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 acgggcgcatcccgcgggggggcgctgctgtccatggacgccttggacctcaccgacaage 322
                                                                                          Gaps
                                                                                                                                23 cggaccgggggggggggggggggagccagagtgggaggaaggcgggggagtccaggttccg 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        383 tgggcctgcaggagatggccgggcagctgcaggcggccacgcaccagggtgagccgccc 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 tggtcagcttctacctggagacctacggcgcgagctcaccgctaacgtgctgcgcgaca
                                        7.9%; Score 49.4; DB 1; Length 18994; ilarity 44.9%; Pred. No. 0.092; Conservative 0; Mismatches 231; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Wayne
STRATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/282,696
FILING DATE: 29-JUL-1994
FILING DATE: 29-JUL-1994
---ANTION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 32,425-00 TELECOMMUNICATION INFORMATION: TELEPHONE: 201-831-3246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08282696
Patent No. 5846806
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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nucleic acid
                                                              Similarity
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                                             Query Match
                                                                 Best Local
Matches 18
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CDS 1165..1992

FEATURE:

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APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Merlo, Donald J.
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Patti J.
APPLICANT: Waldron, clive
TITLE OF INVENTION: Broaghthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                      DB 3; Length 530;
                                                                                                                                                                                                                                                                                                                                                                                                                   143 gggatcctggagccatggggcgcgcgcgacgccatcctggatgcgc 190
                                                                                                                                                    Query Match 7.7%; Score 48; DB 3; Length 530. Best Local Similarity 55.4%; Pred. No. 0.15; Matches 93; Conservative 0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: I LOPPY disk
COMPUTER: TEMPY COMPATIBLE
COMPATIBLY
COMPUTER: TEMPY COMPATIBLE
CLASSIFICATION NUMBER: US/09/036,987A
FELING DATE: 09-MAR-1998
CLASSIFICATION NUMBER: 28,479
REGISTRATION NUMBER: 28,479
REFERENCE/COCKET NUMBER: 50,608
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
TEMPY SEQUENCE CHARACTERISTICS:
LENGTH: 2310 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Indiana
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 25, Application US/09036987A; Patent No. 6143526
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) FEATURE:
; LENGTH: 530 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
TOPOLOGY: linear
US-08-758-662-4
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US-09-036-987A-25
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                                                       Query Match 7.7%; Score 48; DB 3; Length 2310; Best Local Similarity 48.5%; Pred. No. 0.15; Matches 132; Conservative 0; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                        321 gctggtcagcttctacctggagacctacggcg 352
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August 30, 2001, 21:14:47; Search time 81.93 Seconds (without alignments) 4797.588 Million cell updates/sec
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| S1D51/gcgdata/geneseq/geneseqn/NA1983.DAT: |
| S1D51/gcgdata/geneseq/geneseqn/NA1983.DAT: |
| S1D51/gcgdata/geneseq/geneseqn/NA1984.DAT: |
| S1D51/gcgdata/geneseq/geneseqn/NA1985.DAT: |
| S1D51/gcgdata/geneseq/geneseqn/NA1986.DAT: |
| S1D51/gcgdata/geneseq/geneseqn/NA1980.DAT: |
| S1D51/gcgdata/geneseq/geneseqn/NA1990.DAT: |
| S1D51/gcgdata/geneseq/geneseqn/NA1990.DAT: |
| S1D51/gcgdata/geneseq/geneseqn/NA1991.DAT: |
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| S1D51/gcgdata/geneseq/geneseqn/NA1995.DAT: |
| S1D51/gcgdata/geneseq/geneseqn/NA1995.DAT: |
| S1D51/gcgdata/geneseq/geneseqn/NA1999.DAT: |
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         730101 segs, 313950809 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                              nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                      US-09-691-763B-4
626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                              OM nucleic -
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                                                                                                                                                                                                                   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		Human cancer assoc	Human breast tumou	Human CARD-5 cDNA.	Human colon cancer	Mouse CARD-5 cDNA.	Human FLEXHT-30 nu	MEFV gene sequence	FMF associated pro	Human ATLAS-2-enco	Platenolide syntha	Platenolide syntha
SUMMARIES		AAC / / 884	AAZ33631	AAF30007	AAC98638	AAF30008	AAC88099	AAX37084	AAX37085	AAS00033	AAT78508	AAT80414
DB		77	20	22	21	22	22	20	20	22	18	18
% Query Match Length DB ID	1 1	AII	779	740	432	777	807	16891	3512	6461	44377	44377
% Query Match		62.1	58.8	51.4	51.1	28.6	27.9	13.8	11.9	10.9	8.4	8.4
Score	1 6	383	368	322	320	178.8	174.4	86.2	74.8	68.4	52.6	52.6
Result No.		-	7	e	4	S	9	7	ω,	6	10	11

Rosen CA, Ruben SM;

S. cellulosum DNA	al DNA sec	- m	Pseudomonas sp. WF	Amycolatopsis medi	Mature isoamylase	Flavobacterium iso		Full length Flavob		HCMV strain AD169	Epstein Barr Virus	Sequence encoding	Human OCT-T1 parti	Brn-3a polynucleot	Human transcriptio	Saccharopolyspora	Nucleotide sequenc	Human adenosine Al	Central fragment o	Cephamycin biosynt	Streptococcus olea	Maize nitrite redu	Mouse Elf-1 cDNA.	cDNA encoding a ma	rus	Freac11 gene. Hom	M. vaccae antigen	M. vaccae potb gen		Cytochrome P450 cD	ecreted p	Canine betal-adren	
AAA11992			AAA38389	AAV21187	AAT10429	AAV23640	AAT10428	AAV23639	AAV08427	AAV08416	AAX90924	AAN92408	AAA95215	AAX09010	AAA29006	AAZ21502	AAV33912	AAX53491	AAX21398	AAT08693	AAA09469	AAQ12000	AAT15008	AAV42926	AAQ91580	AAX28103	AAV34602	AA211337	AAX26871	AAX26865	22	AAZ98400	
21	- 8 - H	20	21	19	17	19	17	19	20	20	20	10	21	20	21	20	20	20	20	16	21	12	17	19	16	20	13	20	20	20	21	21	
37856	30001	30001	11279	53789	2244	2244	2334	2334	1765	18994	1925	2061	530	1272	1272	2310	4524	114955	2538	2672	50937	1844	1809	1809	15079	2106	861	861	1506	2261	1803	1845	
8.3																																	
51.8	50.8	50.8	50.6	50.6	20	20	20	20	9	49.4	œ	α	48	48	48	48	48	48	47.8	7	47.4	47	46.6	ဖ	46.6	9	9	9	46	46	45.8	45.8	
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## ALIGNMENTS

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RESULT

Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiatrhritic; antiviral; antinflammatory; antityvoid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coaquiant; nockropic; immune disorder; haematopoietic cell disorder; autoimmune disorder; haematopoietic cell disorder; autoimmune disorder; haematopoietic; antiangiogenic; gene therapy; inflammation; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening; ss. Human cancer associated gene sequence SEQ ID NO:278. AAC77884 standard; cDNA; 811 BP. (HUMA-) HUMAN GENOME SCI INC. 99US-0124270. 08-MAR-2000; 2000WO-US05882. (first entry) WO200055350-A1. 12-MAR-1999; Homo sapiens. 08-FEB-2001 21-SEP-2000. AAC77884; 

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This invention decribes novel human nucleic acid sequences from tumor breast tissue which have cytostatic activity. The nucleic acid sequences can be used to produce and isolate full-length gene sequences. They can be used to express proteins, which can be used as tools to find an activity against breast cancer. The sequences can be used in sense or antisease form. They are especially useful for medicaments for gene therapy to treat breast cancer. AAZ33611-448617 represents expressed sequence tags described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gtgccgctgcgcgagggctacgggcgcatcccgcgggggcgcgctgctgttccatggacgcc 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 gigccgcigcgcgagggciacgggcgcatcccgcgggggcgcgctgctgtccaiggacgcc 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ttggacctcaccgacaagctggtcagcttctacctggagacctacgggcgccgagctcacc 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human nucleic acid sequences and protein products from tumor breast tissue, useful for breast cancer therapy \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gatgcgctggagaacctgaccgccgaggagctcaagaagttcaagctgaagctgctgtcg
                                                                                                        tag; EST; human; breast; cancer; gene therapy; cytostatic; medicament; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 779 BP; 149 A; 252 C; 251 G; 127 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.8%; Score 368; DB 20;
Similarity 100.0%; Pred. No. 5e-58;
68; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hinzmann B, Schmitt A, Pilarsky C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                        Human breast tumour-associated EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1a; 101; 188pp; German.
                                                                                                                                                                                                                                                                                                                                                              98DE-1013839.
                                                                                                                                                                                                                                                                                                                                                                                                                    98DE-1013839.
08-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-528981/45.
                                                                                                           Expressed sequence
                                                                                                                                      treatment; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368
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                                                                                                                                                                                               Homo sapiens
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Matches 368;
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                                                                                                                                                                                                                                      In AAB4399 to AAC78448 encode the human cancer associated proteins given in AAB4399 to AAB4429. The proteins can have activities based on the tissues and cells the genes are expressed in Example of activities artisues and cells the genes are expressed in Example of activities antidiabetic; antiasthmatic; antifolator; amunomodulator; antidiabetic; antiasthmatic; antifolator; antiathritic; antidiabetic; antidiator; and antidiator; and antidiator; and antidiator; and antidiator; antidiator and antidiator and antidiator antidiator and antidiator antidiator and antidiato
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                                                                                                           Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ttcaagctgaagctgctgtcggtgccgctgcgagggctacggggcgatcccgcgggggc
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100.0%; Pred. No. 8.6e-62;
ive 0; Mismatches 0;
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                                                                                                                                                                                         Claim 1; Page 841; 2352pp; English.
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                                2000-587533/55
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Query Match

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recruitment domain 5 (CARD-5, see AAB20085). The CDNA was isolated
from a testisa CDNA ilbrary using murithe CARD-1. Plasmid EpHC5
containing CARD-5 cDNA is deposited as ATCC PTA-13. CARD-5
is an intracellular protein predicted to be involved in regulating
caspase activation. It is useful as a modulating agent in
regulating cellular processes include cell growth and cell death.
Methods of diagnosing and treating patients suffering from a
discorder associated with an abnormal level or rate of apoptici
cell death, abnormal activity of the Fas/APO-1 receptor complex,
abnormal activity of a caspase involve administering a compound
that modulates the expression or activity of CARD-5. Cor CARD-6 e.g. a small molecule, antisense nucleic acid, ribozyme
or polypeptide. Such disorders include cancer, viral infection,
autoimmune disorders, neurological diseases, heematological
disorders, inflammatory disorders and immune disorders. CARD
nucleic caids can be used to express CARD proteins in a host cell
ce g. for gene therapy applications, to detect a genetic lession and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated intracellular proteins predicted to be involved in regulating caspase activation are used for diagnosis and treatment of e.g. cancer, viral infections, autoimmune diseases, neurological diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "the open reading frame is also specifically
claimed in Claim 1(a)"
                                                                                                                                                                                                                                                                           CARD-5; caspase recruitment domain; human; cancer; infection; autoimmune disease; nemantological disease; hamantatological disease; inflammation; antitumour; antiseptic; immune disease; antiinflammatory; apoptosis; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
54..641
                                    BP.
                                    AAF30007 standard; cDNA; 740
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                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                      Human CARD-5 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy; ss
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Gaps

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51.4%; Score 322; DB 22; Length 740; 100.0%; Pred. No. 8.7e-50; ive 0; Mismatches 0; Indels (

Matches 322; Conservative

Best Local Similarity

Query Match

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AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53334 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynucleotides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; colon cancer; colon cancer antigen; diagnosis; detection; diagnification; cytostatic; cardioactive; neuroprofective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; ss.
                                                                                                                                                                                                                                                       246
                                                                                 127 tgaagctgctgtcggtgccgctgcgcgagggctacggggcgcatcccgcgggggcgcgctgc 186
                                                                                                                                                                                         349
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170 gegaegecatectggatgegetggagaacetgaecgeegaggageteaagaagtteaage
                                                                                                                             tgaagctgctgtgcgtgccgctgcgcgagggctacggggcgatcccgcggggggcgcgctgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human colon cancer antigen nucleotide sequence SEQ ID NO:648.
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proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, immune gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AABS4007 represent sequences used in the exemplification of the present
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                                                                                                                                                                                                                                                                              128 aagctgctgtcggtgccgctgcgcgagggctacggggcgcatcccgcgggggcgctgctg 187
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89..670
/*tag= "the open reading frame is also specifically
claimed in Claim 1(a)"
                                                                                                                                                                               aagctgctgtcggtgcgctgcgcgagggctacgggcgcatcccgcgggggcgctgctg
                                                                                                                                                                                                   CARD-5; caspase recruitment domain; mouse; cancer; infection; autoimmune disease; neurological disease; immune disease; inflammation; antitumour; antiseptic; immunomodulator; antiinflammatory; apoptosis; diagnosis; gene therapy; ss.
                                                                                                                                         51.1%; Score 320; DB 21; Length 432; 100.0%; Pred. No. 2e-49; 1ve 0; Mismatches 0; Indels (
                                                                                                            Sequence 432 BP; 77 A; 142 C; 152 G; 61 T; 0 other;
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                                                                                                                                                 Best_Local Similarity
Matches 320; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse CARD-5 cDNA.
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                                                                                           invention.
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The present sequence is that of cDNA encoding mouse caspase
recruitment domain 5 (CARD-5, see AA200066). The CDNA was isolated
from a coronary artery smooth muscle cell library using the CARD
domain of RAIDD as probe. Plasmid EpWC5 containing murine CARD-5
CDNA is deposited as ATCC PTA-212. Murine CARD-5 CDNA shows
CGB.2% identity to human CARD-5 CDNA (see AAF30007). CARD-5
is an intracellular protein predicted to be involved in regulating
caspase activation. It is useful as a modulating agent in
regulating cellular processes include cell growth and cell death.
Methods of diagnosing and treating patients suffering from a
disorder associated with an abnormal level or rate of apoptoric
cell death, abnormal activity of the Fas.ABO-1 receptor complex,
abnormal activity of a caspase involve administering a compound
that modulates the expression or activity of CARD-3. CARD-4. CARD-5
or CARD-6 e.g. a small molecule, antisense nucleic acid, ribozyme
or polypeptide. Such disorders include cancer, viral infection,
autoimmune disorders, neurological diseases, heamatchogical
disorders, inflammatory disorders and immune disorders.
CC eg. for gene therapy applications, to detect a genetic lession and
to modulate CARD activity.
                                                                                                                                                                                                                                                                                                                                  Isolated intracellular proteins predicted to be involved in regulating caspase activation are used for diagnosis and treatment of e.g. cancer, viral infections, autoimmune diseases, neurological diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319
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0; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1(a); Fig 19; 208pp; English.
                                                                    (MILL-) MILLENNIUM PHARM INC
99US-0340620
                                                                                                                                                                                                                                                                                                                                                                                                                                              haematological disorders -
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Matches 251; Conservative
                                                                                                                                                                                                                         WPI; 2001-061973/07
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                                                                                                                                            Bertin J;
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152
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                                                                                                                                                                                                                                                       Human, FLEXHT; full-length molecules expressed in human tissue; diagnosis; gene expression; genetic linkage; genetic variability; antianaemic; anticonvulsant; antiarteriosclerotic; immunomodulatory; cytostatic; antiasthmatic; antiinflammatory; hepatotropic; antidiabetic; anti-gout; antihrhumatic; antiinflammatory; hepatotropic; antidiabetic; anti-gout; antipsoriatic antithreumatic; antiuloce; gene therapy; anemais; ouch; epilepsy; arteriosclerosis; atherosclerosis; developmental disorder; concer; immunological disorder; asthma; bronchitis; cirrhosis; crohn's disease; diabetes mellitus; Grave's disease; miltiple sclerosis; outcerative colitis; sa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baughn MR, Yang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human FLEXHT protein and DNA sequences, useful for treating immunological disorders, developmental disorders, and cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 807 BP; 175 A; 253 C; 242 G; 137 T; 0 other;
                                                                                                                                                                                                    Human FLEXHT-30 nucleotide sequence SEQ ID NO:85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yue H, Tang YT, Lal P, Reddy R, Batra S,
Azimzai Y, Lu DAM, Au-Young J, Shih LL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 154; 168pp; English.
AAC88099 standard; cDNA; 807 BP
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99US-0311937.
99US-0311940.
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                                                                                                                             (first entry)
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14-MAY-1999;
14-MAY-1999;
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                                                                                                                                 09-MAR-2001
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Gaps

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Query Match 27.9%; Score 174.4; DB 22; Length 807; Best Local Similarity 77.6%; Pred. No. 2.5e-23; Matches 211; Conservative 0; Mismatches 61; Indels 0;

Query Match

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MEFV gene sequence associated with familial mediterranean fever (FMF).
                                          430
                                                                        tctacctggagacctacggcgccgagctcaccgctaacgtgctgcgcgacatgggcctgc 391
                                     tcccqcgggggcgctgctgtcatggacgccttggacctcaccgacaagctggtcagct
              gagecatgggaacgaagcgcgaggccatcctgaaggtgctggagaacctgacaccggagg
                              MEFV; protein pyrin; Familial Mediterranean Fever; FMF; human; FMF-associated mutant; hereditary disease; colchicine; ss.
                                                                                                                      392 aggagatggccgggcagctgcaggcggccacg 423
                                                                                                                                     551 tggaggaggccgcacggctgcagcgggctgcg 582
                                                                                                                                                                                                                                                                            Location/Qualifiers
1011..14450
/*tag= a
/note= "contains introns"
                                                                                                                                                                          AAX37084 standard; DNA; 16891 BP
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/*tag= 1
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/number= 5
11045..11067
/*tag= 1
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/*tag= i
/number= 4
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10578..11044
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1288..2806
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3440..7812
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/*tag= h
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                              212
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1022 ccctagtgaccatctgctgtccaccctggaggagctggtgccctatgacttcgagaagtt 1081

caagetgaagetgetgteggtgeegetgegegagggetaeggggegeateeegegggggege 284

225

QQ ò g

285

1082 caagttcaagctgcagaacaccagtgtgcagaaggagcactccaggatccccggagcca

1262 ggagetecacagggeagecatteagggtaagegggeecaggeetecte 1312

AAX37085 standard; DNA; 3512 BP.

405 gcagctgcaggcgaccacgcaccagggtgagccgccccgttcccctccac 455

345 ctacggcgccgagctcaccgctaacgtgctgcgcgacatgggcctgcaggagatggccgg

ò qq δ g

1142 gatccagagagccaggccggtgaagatggccactctgctggtcacctactatggggaaga 1201 gctgctgtccatggacgccttggacctcaccgacaagctggtcagcttctacctggagac 344

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The present sequence represents a novel genomic nucleic acid sequence (MEY) encoding the protein pyrin associated with Familial Mediterranean edid encoding pyrin or its FMF-associated mutant, operably linked to a cid encoding pyrin or its FMF-associated mutant, operably linked to a functional promoter, are used for the recombinant expression of the protein. The invention provides a method for diagnosing risk of FMF that comprises analyzing a patient sample for an amino acid or nucleic acid sequence of pyrin; and (b) correlating detection of a mutated sequence with risk of developing FMF Diagnostic Kits developed in this invention are used to identify and treat individuals at risk from FMF, a hereditary disease prevalent in persons having a non-Ashkenazi Jewish, Armenian, atab, or Turkish background. Prior art FMF treatment with colchicine is invention will cover all individuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A new gene, MEFV, associated with Mediterranean Familial Fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16891 BP; 3905 A; 4308 C; 4316 G; 4356 T; 6 other;
                                                                                                                                                                                                                    /cons_splice (5'site Yes, 3' site No) 13701..13731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aksentijevich I, Blake T, Centola M, Collins FS;
Deng Z, Doggett NA, Fischel-ghodsian N, Gumucio DL;
Kastner DL, Liu PP, Pras M, Richards RI, Ricke DO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                /*tag= p
/number= 8
13338..13700
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                                                                                                           /*tag= o
/number= 7
13305..13337
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13732..13896
/*tag= s
/number= 9
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/number= 7
13119..13304
/*tag= o
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/*tag= t
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13003..13118
/number= 6
11068..13002
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/number= 8
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P-PSDB; AAX09001.
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MEFV; protein pyrin; Familial Mediterranean Fever; FMF; human; FMF-associated mutant; hereditary disease; colchicine; ss.

Location/Qualifiers

Key

Homo sapiens

FMF associated protein pyrin encoding cDNA.

(first entry)

05-JUL-1999

AAX37085;

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The invention provides a novel genomic nucleic acid sequence (MEFV)
                                                                                                                                                        /note- "sequence coding for bZIP transcription factor basic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                          A new gene, MEFV, associated with Mediterranean Familial Fever
                                                                                                                                                                               /*tag= c
/note= "sequence coding for Robbins/Dingwall
consensus nuclear targeting signal"
1769..2309
                                                                                                                                                                                                                         /*tag= d
/note= "coding for rfp, or B30.2 domain"
                                                                                                                                                                                                                                                                                                                                               Aksentijevich I, Blake T, Centola M, Collins FS;
Deng Z, Doggett NA, Fischel-ghodsian N, Gumucio DL;
Kastner DL, Liu PP, Pras M, Richards RI, Ricke DO;
                                                                                                                         /product= "pyrin protein"
837..880
                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Fig 2; 49pp; English.
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P-PSDB; AAY09001.
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Gaps

Score 86.2; DB 20; Length 16891; Pred. No. 1.5e-07; 0; Mismatches 128; Indels 0;

0,

Query Match 13.8%; Best Local Similarity 56.0%; Matches 163; Conservative 0

165

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cgcgcgcgacgccatcctggatgcgctggagaacctgaccgccgaggagctcaagaagtt 224

Homo sapiens.

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cencoding the protein pyrin associated with Familial Mediterranean Ever (FMF). Host cells transformed with a vector comprising a nucleic acid encoding pyrin or its PMF-associated mutant, operably linked to a functional promoter, are used for the recombinant expression of the comprises analyzing a patient sample for an amino acid or nucleic acid sequence of pyrin; and (b) correlating detection of a mutated sequence with risk of developing FMF: Diagnostic kits developed in this invention are used to identify and treat individuals at risk from FMF, a hereditary disease prevalent in persons having a non-Ashkenazi Jewish, Armenian, Arab, or Turkish background. Prior art FMF treatment with colchicine is not effective in patients who are colchiciner resistant, and this convention will cover all individuals. The present sequence represents the corresponding cDNA sequence (designated V75-1) of the MEFV genomic
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cytokine receptor; autoimmune disorder; immune disorder; cancer;
T-lymphocyte-associated disorder; cell-proliferation disorder; tumour;
cell differentiation disorder; immune deficiency disorder; malignancy;
viral infection; bacterial infection; fungal infection; metabolism;
chromosome 11p15.5; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 ggagetecacagggeagecatteaggaatattecacacaagaaaacggeacagatgatte 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 ccctagtgaccatctgctgtccaccctggaggagctggtgccctatgacttcgagaagtt 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 caagetgaagetgetgteggtgeegetgegegagggetaeggggegeateegggggggege 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 caagttcaagctgcagaacaccagtgtgcagaaggagcactccaggatccccggagcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   getgetgtecatggacgcettggaceteacegacaagetggteagettetaeetggagae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 ctacggcgccgagctcaccgctaacgtgctgcgcgacatgggcctgcaggagatggccgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  525 ctaaacaaagctgctctaccggaaaggaggctccccacgcttggcctaccgaccaacggg
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Pred. No. 1.7e-05;
0; Mismatches 242; Indels 0;
                                                                                                                                                                                                                                                                                                                                                             Sequence 3512 BP; 843 A; 966 C; 996 G; 707 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        585 accccggccccacggcgggaagggaagggaaggggatcactt 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 473 cagccagcccgaggccgggagggggctgtcgaggaagcccct 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS00033 standard; cDNA; 6461
                                                                                                                                                                                                                                                                                                                                                                                                                              11.9%;
47.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 47.6 Matches 220; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Best Local S
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The sequence encodes human activated T-lymphocyte associated sequence 2, ATLAS-2. ATLAS-2 is related by homology to cytokine receptors and its gene is located on chromosome 11p15.5. ATLAS proteins, polynucleotides and antibodies are useful for treating/preventing conditions associated with an autoimmune disorder, immune disorder, T-lymphocyte-associated disorder, cell-proliferation disorder, cell differentiation disorder. To disorder, cell-proliferation disorder and immune deficiency disorder and for screening for a modulator of activity or of latency or predisposition to an immune disorder.

CC ATLAS proteins, polynucleotides and antibodies are useful in therapeutic or prophylactic treatment of diseases associated with cell-proliferation gene, to modulate ATLAS activity, to screen drugs or compounds that condulate ATLAS activity, to screen drugs or compounds that condulate ATLAS activity, to screen drugs or compounds that condulate ATLAS activity or expression and to treat disorders characterised by insufficient or excessive production of ATLAS protein forms that have decreased or aberrant conduction, isolation and detection of ATLAS and to monitor protein containing in tissue. ATLAS is useful for treating/preventing infection by bacteria, viruses and fungi, affecting bodily characteristics, e.g.

C containing the polynucleotide is useful to produce non-human transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated activated T lymphocyte associated sequences for treating or preventing immune system associated disorders such as autoimmune disorder, immune disorder, and T-lymphocyte-associated disorder \cdot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 caagaagttcaagctgaagctgctgtcggtgccgctgcgaggggtacggggcgatcc 275
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Pred. No. 0.00023;
0; Mismatches 116;
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                               Location/Qualifiers
1..5556
                                                                                /product= "ATLAS-2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.9%;
Best Local Similarity 55.8%;
Matches 154; Conservative
                                                                                                                                                                                                                             20-AUG-1999; 99US-0150105.
28-APR-2000; 2000US-0560101.
28-APR-2000; 2000US-0560345.
28-APR-2000; 2000US-0560948.
28-APR-2000; 2000US-0560948.
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                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                  platenolide
polyketide;
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Matches 100;
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8888888888888
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                                                                                                                                                                                                                                                                                            This sequence represents the platenolide synthase gene cluster of the invention. This sequence is referred to as the srm6 gene, and was isolated from Streptomyces ambofaciens. This sequence encodes the multi-functional proteins which direct the synthesis of the polyketide
     276 gcggggggggcgctgtccatggacgccttggacctcaccgacaagctggtcagcttcta 335
                                          cctggagacctacggcgccgagctcaccgctaacgtgctgcgcgacatgggcctgcagga 395
                                                          216 cggcccggagcctgccctggaggtggcccgcaagaccctcaagagggcggacgcgcga 275
                                                                                                                                                                                                                  Platenolide synthase gene cluster; platenolide production; srmG gene; multi-functional protein; macrolide antibiotic; spiramycin; ss.
                      DNA encoding Streptomyces ambofaciens platenolide synthase domain for production of spiramycin-related polyketide antibiotics
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/note= "ORF1 encodes protein shown in AAW23716"
14046..20036
                                                                                                                                                                                                                                                                                                                                                                                    /note= "ORF4 encodes protein shown in AAW23719"
36155..41830
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"ORF5 encodes protein shown in AAW23720"
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in AAW23718"
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/transl_except= (pos:20111..20113, -/
/note= "ORF3 encodes protein shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Richardson MA;
                                                                             396 gatggccgggcagctgcaggcggccacgcaccaggg 431
                                                                                              276 cgtggcggcgcagctccaggagcggcggctgcagcg 311
                                                                                                                                                                                                                                                              Location/Qualifiers
350..14002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rao RN,
                                                                                                                                                                                               Platenolide synthase gene cluster.
                                                                                                                                            BP.
                                                                                                                                          AAT78508 standard; DNA; 44377
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20110.31284
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                                                                                                                                                                                                                                             Streptomyces ambofaciens
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Rosteck PR;
                                                                                                                                                            AAT78508;
                                         336
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platenolide. Platenolide is the basic building block of the macrolide antibiotic spiramycin. The DNA can be used to produce compounds exhibiting antibiotic activity based on the platenolide structure, including specifically the macrolide antibiotic spiramycin analogues and derivatives. Modifications of the platenolide synthase DNA sequence can be made so as to change the number and type of carboxylic acids incorporated into the growing polyketide chain and to change the kind of post-condensation processing that is conducted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16903 ggcccaggacggacgggctgtcggcggcgggtctgcgcgaggtggagcacccctgctca 16962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389 tgcaggagatggccgggcagctgcaggcggccacgcaccagggtgagccgccccgttcc 448
                                                                                                                                                                                                                                                                                                                                                                                                                   329 gettetacetggagacetacggegeeggegeteacegetaacgtgetgegegacatgggee 388
                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          449 cctccacccgtctttcccctccacccagcgctttaccccggggctcttccgct
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/note= "ORF1 encodes protein shown in AAW22606"
14046..20036
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in AAW22608"
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encodes protein shown
                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                 79;
                                                                                                                                                                                                                                                                                                           Score 52.6; DB
Pred. No. 0.15;
0; Mismatches
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36155..41830
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/note= "ORF5
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This invention describes a novel DNA sequence (I) whose expression products effect or are involved in the enzymatic biosynthesis, mutasynthesis or partial synthesis of polyketide or heteropolyketide compounds (II). (I) can be inserted into an expression vector and used to transform or transfect prokaryotic or eukaryotic cells with the aim of obtaining strains that produce large amounts of polyketide or heteropolyketide compounds, especially epothilones, which have cytotoxic and/or immunosuppressant and antiblotic and antifungal activities and are useful as plant-protection agents. This sequence represents the DNA sequence isolated from Sorangium cellulosum which is described in the
                                /product= "ORF3-aminotransferase"
/note= "AGT start codon given in the specification"
9855..11393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA sequence coding for products involved in the biosynthesis of polyketide or heteropolyketide compounds, especially epothilone
                                                                                                                                    "ORF4- tyrosine/DOPA-Decarboxylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "ORF13-transcription regulator"
complement (35730..36242)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "ORF14-transcription regulator"
/note= "GTG start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "ORF10-transcription regulator"
                                                                                                                                                                                                             :t= "ORF5-3-oxoacyl-ACP-reductase"
"ACC start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "ORF11-regulation element"
                                                                                                                                                                                                                                                                                          "ORF6-polyketide synthase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "ORF12-regulation element"
complement (35255..35616)
                                                                                                                                                                                                                                                                                                                                               "ORF7-peptide synthetase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "ORF9-regulation element"
                                                                                                                                                                                                                                                                                                                                                                                                         /product= "ORF8-transpeptidase"
complement (30040..31720)
/product= "ORF2-monooxygenase"
complement (8433..9550)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "GTG start codon"
33661..34077
                                                                                                                                                     /note= "GTG start codon"
12212..13658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "CGC stop codon
31982.,32932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 20-33; 36pp; German.
                                                                                                                                                                                                                                                                                   /product= "ORE
20003..27889
/*tag= q
                                                                                                                                                                                                                                    /note= "ACC s
L5374..19984
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                                                                                                                                                                                                                                                                                                                                                                     28251..29400
/*tag= h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-294101/26.
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  This sequence represents the platenolide synthase gene cluster of the invention. This sequence is referred to as the srmG gene, and was isolated from Straptomyces ambofaciens. This sequence encodes the multi-functional proteins which direct the synthesis of the polyketide platenolide. Platenolide is the basic building block of the macrolide at thiotic spiramycin. This sequence was used along with the ty1G gene (see AATB0415) to create a hybrid ORF1 sequence (see AATB0415). The ty1G gene is the tylactone synthase gene cluster of the invention. The ty1G gene is the tylactone synthase gene cluster of the invention. The ty1G gene is the tylactone is the basic building block of the antibiotic tylactone. Tylactone is the basic building block of the antibiotic tylosin. The hybrid sequence can be used to transform S. ambofaciens lacking the srmG ORF1 sequence, or S. fradiae lacking the ty1G ORF1 sequence, or S. fradiae lacking the ty1G ORF1 sequence, or alter the type of carboxylic acids incorporated, the number of carboxylic acids incorporated and/or the post-condensation reactions performed, thereby resulting in novel tylosin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polyketide biosynthesis; heteropolyketide biosynthesis; mutasynthesis; epothilone; cytotoxic; immunosuppressant; antibiotic; antifungal; plant-protection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16963 ccgccgccgtggaactgcccggcaccgacaccgaggtgtggaccggccgcatatccgct 17021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        389 tgcaggagatggccgggcagctgcaggccacgcaccagggtgagccgccccgttcc 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             329 gettetacetggagacetacggegeegageteacegetaacgtgetgeegacatgggee 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449 octocaccccgtctttcccctccacccacaccagcgcttaccccgcggggctcttccgct 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cellulosum DNA encoding polyketide and hereropolyketide enzymes
                                                                                                                   DNA encoding Streptomyces fradiae tylactone synthase domain - for production of tylosin-related polyketide compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 44377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79; Indels
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Pred. No. 0.15;
0; Mismatches 79;
                     Sutton KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "ORF1-tRNA synthetase"
/note= "gtg start codon"
complement (6374..7111)
/*tag= b
                                                                                                                                                                         Example 2; Pages 110-134; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (3398..6100)
                     Rosteck PR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA11992 standard; DNA; 37856 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.4%;
Best Local Similarity 55.9%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-AUG-2000 (first entry)
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                                                       WPI; 1997-418046/39.
P-PSDB; AAW22606-W22610.
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                   Dehoff BS,
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us-09-691-763b-4.rng

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WPI; 1996-105220/11.
                        P-PSDB; AAR92747
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                                                                                                                                                                                                                                                                                                               Query Match
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AAT61016/c
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                                                                                                                                                           31614 TGGAGGAGCGCTTCTTCGCCGCCGGCGAGGACCGCCTCCCCGAGGTCGAGTACCGCGTCG 31555
                                                                                                                                                                                                     31554 ATCGCGACGGCCTCGCGCGCGC----GTCGCCGAGCTGCGCGAGCTCCTCGGGGCCATC 31499
                                                                                                                                                                                                                                             31498 GACGGGGACGCGCCGCCCCGCCTGGCTGCGGGACAACGTCCGCGCGCAGATCCAGGCC 31439
                                                                                                                                                                                                                                                                                                                                 31378 GGCGCGCGCGCTCGCGGTTCTTCGGCGCTCGCTCAGGAACATCGACCTCGCCGAGCAC 31319
                                                                                                                                                                                                                                                                                                                                                                         31318 CTCACCGAGCGCCTGCGCGTCCACGCTGGGACGAGGCCAGCGATCCCGAGGAGGAGCCG 31259
                                                                                                                                      64 gcggggagtccaggttccgccccggagccgacttcctcctggtcggcggctgcagcgggg 123
                                                                                                                                                                                gatgcgctggagaacctgaccgccgaggagctcaagaagttcaagctgaagctgctgtcg 243
                                                                                                                                                                                                                                                                  244 gigccgcigcgcgagggctacggggcgcatcccgcgggggcgcgct---gcigiccatggac 300
                                                                                                                                                                                                                                                                                                             gccttggacctcaccgacaagctggtcagcttctacctggagacctacggcgccgagctc 360
                                                                                                                                                                                                                                                                                                                                                    361 accgctaacgtgctgcggacatgggcctgcaggagatggccggggcagctgcaggcggcc 420
                                                                           Gaps
                                                                                             7;
                                                      Length 37856,
                   Sequence 37856 BP; 5655 A; 13666 C; 12913 G; 5622 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         simian monkey SA\theta virus gB glycoprotein; immunoassay; sls; herpes B virus; ss.
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Black D, Eberle R, Hilliard J, Scinicariello F;
                                                    Score 51.8; DB 21;
Pred. No. 0.21;
0; Mismatches 232;
                                                                                                                                                                                                                                                                                                                                                                                                             31258 CTCGACGCCGCCTCCGGGACATGCTCGCCGCCC 31222
                                                                                                                                                                                                                                                                                                                                                                                               421 acgcaccagggtgagccgccccgttcccctccaccc 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SA8 virus gB glycoprotein coding sequence.
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/product= gB_glycoprotein
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87..2744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
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                                                  8.38;
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                                                             Best_Local Similarity *'...
Matches 218; Conservative
method of the invention.
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                                                    Query Match
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This sequence encodes the herpes simian monkey SAB virus gB captories. Such sequences have been used to develop synthetic glyoprotein. Such sequences have been used to develop synthetic DNA primers which have homologous sequences of conserved regions which flank a divergent region of the gB glycoprotein gene. In addition, proteins such as the gB glycoprotein have potential use in the development of serological immunoassays. One approach is to synthesize peptides which, based on the properties of the predicted proteins sequence, are likely to be immunologically active. Such peptides can be used as substrate antigens in immunoassays to detect sequence and any also be used to produce antibodies against specific regions of the gB glycoprotein which are unique to one virus. These can then be used to develop virus-specific immunoassays for differentiation of SAB virus from other primate alpha-herpes viruses and for identification of antibodies directed against SAB virus in primate serum samples.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccccggagccgacttcctcctggtcggcggctgcagcggggtgagcggcggcagccg
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Detection of herpes B virus by PCR amplification of sample DNA detect a specific herpes simian monkey B virus DNA segment.
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44.5%; Pred. No. 0.28;
tive 0; Mismatches 253; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2943 BP; 462 A; 1103 C; 983 G; 395 T; 0 other;
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Matches 203; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24201 GCTCGCCGACGCGGGGGGGGGACCCGACGACGATGCCGGACTTCTCCGCCGCGCGTCGTGAC 24142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24381 CTGGGACGCCACACTGGCGGGCCGGTCCGGTCTCGGGCCGCTGACCCGCTTCGACTCCAC 24322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cttggacctcaccgacaagctggtcagcttctacctggagacctacggcggcgagctcac 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cgctaacgtgctgcggcgacatgggcctgcaggagatggccgggcagctgcagggggccac 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ggcggggagtccagttccgccccggagccgacttcctcctggtcggcggctgcagcggg 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the total DNA sequence from cosmid clones LP(2)127 and LP(2)128, which contains a Streptomyces aureofáciens (ATCC 13899) DNA that encodes the proteins of the entire chlortetracycline biosynthetic pathway. The biosynthetic gene, which can be expressed in heterologous hosts, especially S. lividans, may be useful in the production of antibiotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 30001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding tetracycline biosynthetic pathway proteins - specifically from Streptomyces aureofaciens for expression in heterologous hosts, specifically S. lividans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 30001 BP; 4055 A; 10939 C; 11019 G; 3988 T; 0 other;
Total DNA sequence from cosmid clones LP(2)127 and LP(2)128
                                                   Cosmid clone; LP(2)127; LP(2)128; chlortetracycline; blosynthetic pathway; recombinant; production; antibiotic; heterologous host; Streptomyces lividans; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.1%; Score 50.8; DB 18; Length 345.6%; Pred. No. 0.32; Asitye 0; Mismatches 257; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lotvin JA, Ryan MJ, Strathy N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Columns 17-44; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       93US-0125468.
90US-0558039.
90US-0558040.
92US-0821109.
92US-0821419.
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                                                                                                                                                                                                                                                                                                                                      90US-0558039
                                                                                                                                                                    Streptomyces aureofaciens
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les 219; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-076853/07.
                                                                                                                                                                                                                                                                                                                                                                                          22-SEP-1993;
26-JUL-1990;
26-JUL-1990;
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                                                                                                                                                                                                                           US5589385-A.
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The invention relates to combination of two plasmids for cloning the genes encoding the biosynthetic production pathways of chlortetracycline, retracycline, or their derivatives. One plasmid contains an origin of replication, an actinomycete (such as Streptomyces lividans, S. ariseofuscus, or S. ambofaciens) active antiblotic resistance gene and ctinomycete active origin of replication and three or more tandem cohesive end sites. The second plasmid contains an actinomycete active origin of replication and three or more tandem cohesive end sites. The invention can be used to clone a large amount of genetic material for the heterologous production of the antibiotics, chlortetracycline, tetracycline and their analogues. A cluster of genes can be inserted into the plasmid allowing a blosynthetic pathway to be transferred in its entirety to a heterologous host. The invention is specifically relates to cloning of the entire tetracycline and second its analogues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chlortetracycline from Streptomyces aureofaciens and its expression in a heterologous host such as S. lividans. The present sequence represents a S. aureofaciens DNA sequence from the cosmid clones designated LP2-127
                                                      24141 GGCCGCCTCGGCCGCCGCCTTCGAGTTCGGCCAGAAGGAACTCCAGGCGCTGTGGAGCAA 24082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Two plasmids for cloning the biosynthetic pathways of tetracycline, chlortetracycline, and their derivatives - comprise an origin of replication, cohesive end sites and optionally, an antibiotic
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                                                                                                                                                                                                                                                                                                                     Chlortetracycline; tetracycline; biosynthetic; actinomycete; S. ariseofuscus; S. ambofaciens; antibiotic resistance gene; S. lividans; S. aureofaciens; cosmid clone; antibiotic; ss.
                                                                                                                                                                                                                                                                                    S. aureofaciens DNA in cosmid clones LP2-127 and LP2-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lotvin JA, Ryan MJ, Strathy
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92US-0821419.
95US-0474933.
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90US-0558040.
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Conservative

Best Local Similarity Matches 219; Conserv

Query Match

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Length 30001;

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AF184072 Homo sapi AC009088 Homo sapi AR017270 Sequence AB023416 Homo sapi AF255794 Homo sapi AF184073 Homo sapi AX082246 Sequence AK000211 Homo sapi

Description

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1190. .2460
  Submitted (09-SEP-1999) Radiation Oncology, Emory University of Medicine, 145 Edgewood Avenue, SE, Atlanta, GA 30335, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 agcgccttttgctggagggcaacggaccggggcggggagtcgggagaccagagtgggagg
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/gene≕"TMS1"
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AXO82258 Sequence
AK3032249 Mus muscu
AF310104 Mus muscu
AF086332 Homo sapi
AXO80915 Sequence
AC009088 Homo sapi
AXO80260 Sequence
AC003175 Homo sapi
AXO82260 Sequence
AF111163 Homo sapi
AF01317 Streptomy
AXO88208 Sequence
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AXO80317 Streptomy
AF015416 Homo sapi
AXO88208 Sequence
AXO80408 Homo sapi
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AC016091 Homo sapi
AC016093 Homo sapi
AC016091 Homo sapi
AC01877 Homo sapi
AC01877 Homo sapi
AC01871 Homo sapi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Activation of a caspase-9-mediated apoptotic pathway by subcellular redistribution of the novel caspase recruitment domain protein TMS1 Cancer Res. 60 (22), 6243-6247 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TMS1, a novel proapoptotic caspase recruitment domain protein, is a target of methylation-induced gene silencing in human breast
                                                                                                                                                                                                                                                                                                                                                                                                                                               AF184072 2821 bp DNA PRI 02-FEB-2001
Homo sapiens target of methylation-induced silencing 1 (TMS1) gene,
complete cds.
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Conway, K.E., McConnell, B.B., Bowring, C.E., Donald, C.D., Warren, S.T.
and Vertino, P.M.
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                                         AB032249
AF310104
HUMZD54H05
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AX082260
AX111163
AC009115
HSAJ03147
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AF018080
AX088215
AX088208
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AC007565
GGPGR
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AC020937
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Vertino, P.M.
Direct Submission
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Unpublished
2 (bases 1 to 233425)
DOE Joint Genome Institute.
Direct Submission
Submitted (03-4099) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 18, 2000 this sequence version replaced gi:7689912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 233425)
DOB Joint Genome Institute.
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Consensus quality: 229603 bases at least Q30
Consensus quality: 23160 bases at least Q30
Estimated insert size: 252540; agarose-fp estimation
Estimated insert size: 233025; sum-of-contigs estimation
Quality coverage: 7.01 in Q20 bases; agarose-fp estimation
quality coverage: 7.6 in Q20 bases; sum-of-contigs estimation
enorge: This is a "working draft" sequence. It currently
e consists of 10 contigs. Gaps between the contigs
ear represented as runs of N. The order of the pieces
                                    1460 ACCGCTAACGTGCTGCGCGACATGGGCCTGCAGGAGATGGCCGGGCAGCTGCAGGCGGCC 1519
                                                                                                                                                                                                                                                                                               1280 CTGGATGCGCTGGAGAACCTGACCGCCGAGGAGCTCAAGAAGTTCAAGCTGAAGCTGCTG 1339
                                                                                                                                                                                           acegctaacgtgctgcgcgacatgggcctgcaggagatggccgggcagctgcaggcggcc 420
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                                                                                                                                      301 gccttggacctcaccgacaagctggtcagcttctacctggagacctacggcgccgagctc
                                                                                                                                                                                                                                                                        421 acgcaccagggtgagccgccccgttcccctccaccccgtcttcccctccaccacacc
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Center Code: JGI
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Homo sapiens chromosome 16 cl
SEQUENCE, 10 ordered pieces.
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10930 AAGGCGGGGAGTCCAGGTTCCGCCCCGGAGCCGACTTCCTCCTGGTCGGCGCGCTGCAGCG 10989
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* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 3768 37767 gap of unknown length
* 3768 4777; gap of unknown length
* 64794 64893; gap of unknown length
* 64794 64893; gap of unknown length
* 64794 64893; gap of unknown length
* 64894 96964; contig of 27026 bp in length
* 97065 119624; contig of 22560 bp in length
* 119625 119524; contig of 22560 bp in length
* 119725 155521; contig of 38797 bp in length
* 15552 155521; contig of 38797 bp in length
* 15552 175996; contig of 1875 bp in length
* 17597 17596; contig of 1875 bp in length
* 17597 17596; contig of 188 bp in length
* 176085 208395; contig of 32311 bp in length
* 223735 223834; gap of unknown length
* 223735 233735 23484; contig of 15239 bp in length
* 223735 233735 23343; gap of unknown length
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                                                                                                                                   is available and
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60156 c 60134 g 56015 t 901 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
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/genra- /genra
              AB023416 782 bp mRNA PRI 18-OCT-2000 Homo sapiens ASC mRNA for apoptosis-associated speck-like protein containing a CARD, complete cds.
                                                                                                                                                                                                                                                                                                         Maximoto,J., Taniguchi,S., Ayukawa,K., Sarvotham,H., Kishino,T., Niikawa,N., Hidaka,E., Katsuyama,T., Higuchi,T. and Sagara,J. ASC, a novel 22-kDa protein, aggregates during apoptosis of human promyelocytic leukemia HL-60 cells
J. Biol. Chem. 274 (48), 33835-33838 (1999)
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                     Homo sapiens cDNA to mRNA
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87. 674
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 779)
Schmitt.A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
Pilarsky,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human nucleic acid sequences from tissue of breast tumors
Patent: WO 9947669-A 21 23-SEP-1999;
SCHAITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHALL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
(DE); FLARRSKY CHRISTIAN (DE)
Location/Qualifiers
                                                                      gcggggagtccaggttccgcccgggagccgacttcctcctggtcggcggctgcagcgggg 123
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Best Local Similarity 100.0%; Pred. No. 1.2e-43;
Matches 368; Conservative 0; Mismatches 0;
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Sequence 21 from Patent W09947669.
AX017270
AX017270.1 GI:10042188
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/db_xref="taxon:9606"
1252 c 251 g 127
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Homo sapiens
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Bukaryota, Metrazoa, Primates; Catarrhini; Hominidae, Homo.
Mammalia, Eutheria, Primates; Catarrhini; Hominidae, Homo.
1 (bases 1 to 770)
McConenell, B. B. and Vertino, P. M.
Activation of a caspase-9-mediated apoptotic pathway by subcellular redistribution of the novel caspase recruitment domain protein TMS1
2055140
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2 (bases 1 to 770)
Conway K.E., McConnell, B.B., Bowring, C.E., Donald, C.D., Warren, S.T. and Vertino, P.M.
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Direct Submission
Submitted (09-SEP-1999) Radiation Oncology, Emory University School
of Medicine, 145 Edgewood Avenue, SE, Atlanta, GA 30335, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF184073 770 bp mRNA PRI 02-FEB-2001
Homo sapiens target of methylation-induced silencing 1 (TMS1) mRNA,
complete cds.
AF184073.1 GI:9863863
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/clone=lib="Soares breast 3NbH8st; NCI_CGAP_Ut3 uterine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="involved in apoptosis" / functe="target of methylation-mediated gene silencing in
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                                 Indels
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Vertino, P.M.
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/product="taget of methylation-induced silencing-1"
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/db_xref="GI:9802276"
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LSMDALDLIDKLVSFYLETYGRELTANVLENMGLOGAATHOGIHFIDOHRA
LIARVTNVEMLLDALYGKVLTDEQYQAVRAEPTNPSKMRKLFSFTPAMNWTCKDLLLQ
ALRESOSYLVEDLERS"
                                                                                                                                                                                                                                                                                                                                                                                                                                Activation of a caspase-9-mediated apoptotic pathway by subcellular redistribution of the novel caspase recruitment domain protein TMS1 Cancer Res. 60 (22), 6243-6247 (2000)
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Submitted (13-APR-2000) Radiation Oncology, Emory University School
of Medicine, 145 Edgewood Avenue, SE, Atlanta, GA 30335, USA
                                                                                                                                                                                               AF255794 713 bp mRNA PRI 02-FEB-2001 Homo sapiens target of methylation-induced silencing-1 (TMS1) mRNA, complete cds, alternatively spliced.
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Conway, K.E., Wacconnell, B.B., Bowring, C.E., Donald, C.D., Warren, S.T.
and Vertino, P.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TMS1, a novel proapoptotic caspase recruitment domain protein, is target of methylation-induced gene silencing in human breast
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 713)
McConnell, B. and Vertino, P.M.
                                   241 TCACCGACAAGCTGGTCAGCTTCTACCTGGAGACCTACGGCGCCCGAGCTCACCGCTAACG 300
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/organism="Homo sapiens"
/db_xref="taxon 9606"
/chromosome="16"
/map="16011.2-p12.1"
/cell_line="Hs598Bst"
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1. .713
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/gene="TMS1"
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Unpubblished (2000)

Sugano, S. Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,
Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,
Shibahara, T., Tanaka, T. and Nakamura, Y.
Direct Submission

Nictic Submitsed (15-FEB-2000) to the DDBJ/EMBL/Genbank databases. Sumio
Sugano, Institute of Medical Science, University of Tokyo, Deptment
of Virology: Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:cdnal@ins.u-tokyo.ac.jp, Tel:13-5449-5286,
NEDO human conAs agenering project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Blotechnology; cDNA library
construction, $\frac{\pi}{2}$ = $\frac{\pi}{2}$ = 3'-end one pass sequencing: Departent of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo septens colon mucosa cDNA to mRNA, clone_lib:ColF clone:COLF1505.
                                                                           Indels
                                       Length
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Homo sapiens cDNA FL320204 fis, clone COLF1505.
AK000211
AK000211.1 G1:7020146
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                                   tch 51.4%; Score 322; DB 10; al Similarity 100.0%; Pred. No. 4.2e-37; 322; Conservative 0; Mismatches 0;
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PPQSAAKPGLHFTDOHRAALIARVTAVVBWLLDALYGKVLTDEQYQAVRAEPTNPSKMR
KLFSFTPANNWTCKDLLLQALRESQSYLVEDLERS"

247 c 241 g 125 t
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Novel molecules of the card-related protein family and uses thereof Patent: WO 0100886-A 48 04-JAN-2001;

Millennium Pharmaceuticals, Inc. (US)

Location/Qualifiers

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PPQSAARFGLHFIDOHRAALIARVTNVEWLLDALYCKVLTDEQYQAVRAEPTNFSKMR
KLFSFTPANNWTCKDLLLQALRSQSYLVEDLERS"
238 c 120 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 740)
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Pred. No. 4.8e-40;
0; Mismatches 4; Indels
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Sequence 48 from Patent W00100826.
AX082246
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/db_xref="taxon:9606"
sapien tumors
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/processin_id="Aag30286.1"
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PPQSAARCGLHFIDOHRAALIARVTNVEWLLDALYGKVLTDEQYQAVRAEFTNPSKMR
KLFSFTPANWTCKDLLLQALESGSGSTLVEDLERS"
221 c 210 g 115 t
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E 2 (bases 1 to 712)

S Martinon, F., Hofmann, K. and Tschopp, J.

Direct Submission

L Submitted (28-SEP-2000) Institute of Biochemistry, University of Lausanne, Ch des Boveresses 155, Epalinges 1066, Switzerland

Location/Qualifiers

1. 712

/organism="Homo sapiens"
/db_xref="taxon:9606"
/ 1. 588
//Otte="contains PYD and CARD domains"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Gaps
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Martinon, F., Hofmann, K. and Tschopp, J.
Pycard a PYD and CARD containing molecule
                                                                                                                                                                                                                                                                                                                                                                                                                   AF310103 712 bp mRNA
Homo sapiens PYCARD mRNA, complete cds.
AF310103
                                                                                                                                                                                                                                                                                                   241 ATGCCGGGCAGCTGCAGGCGGCCACGCACGGG 275
                                                                                                                                                                                                                                                                          397 atggccgggcagctgcaggcggccacgcaccaggg 431
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Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 585)
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Pred. No. 4.1e-34;
0; Mismatches 0; Indels
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Sequence 50 from Patent WO0100826.
AX082248 GI:13171009
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188 c 195 g 91
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Best Local Similarity 99.4%;
Matches 313; Conservative
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/protein_id="cac33150.1"
//db_xref="G1:3317017"
//db_xref="G1:3317017"
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AQSTARTGHEVDQHROALIARVTEVDGYLDALHGSVLTEGGYQAVRAETTSQDKWRKL
FSFPSWWITCRGDLQALKETHPYLVMDLEGS"
193 c 217 9 155 t
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                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 777)
                 140 ccggggatcctggagcatggggcgcgcgcgcgcgcatcctggatgcgctggagaacc 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="unnamed protein product" /codon_start=1
                                                                                                                                                                                                                                 AX082258 777 bp DNA
Sequence 60 from Patent WO0100826
AX082258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"/db_xref="taxon:10090"
89. .670
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1. .777
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Best Local Similarity 70.9%;
Matches 251; Conservative C
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Location/Qualifiers
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/db.xref="G1335316"
/translation="MGRARDAILDALENLTABELKKFKLQAATHOGSGAAPAGIOAPP
QSAARFCHFIDOHRAALTARYTNVEWILDALYGKVLTDEGYQAVRAEFTNPSKMRKL
PSFTPRAWNTCKDLIQALEGGSYLVEDLERS"
229 c 256 g 115 t
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
ODNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequenching by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadam@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                             Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Euthoria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 768)
                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (12 MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                           BCC004470 768 bp mRNA PRI
Homo sapiens, clone MGC:10332, mRNA, complete cds.
BCO04470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH10B-R"
                                      397 atggccgggcagctgcaggcggccacgcaccaggg 431
                                                            241 ATGGCCGGGCAGCTGCAGGCGGCCACGAGGG 275
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246. .653
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99.6%; Pred
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PSFVPSWNLTCKDSLLQALKRIHPYLVMDLEQS"
185 c 206 g 144 t
                                                                                                                                                                                                                                                                                   Masumoto,J., Sagara, J. and Taniguchi,S.

Direct Submission

Submitted (00-Sagara). the DDBJ/EMBL/GenBank databases. Junya
Submitted (00-Sagara) to the DDBJ/EMBL/GenBank databases. Junya
Masumoto, Shinshu University School of Medicine, Research Center on
Aging and Adaptation; Asahi 3-1-1, Matsumoto, Nagano 390-8621,
Japan (E-mail:masumoto@sch.md.shinshu-u.ac.jp, Tel:81-263-37-2723,
Fax:81-563-37-2724)
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                                                                                                                                                                                                  Masumoto, J., Taniguchi, S., Nakayama, K., Ayukawa, K. and Sagara, J. Murine ortholog of ASC, a CARD-containing protein, self-associates, and exhibits restricted distribution in developing mouse embryos Exp. Cell Res. (2000) In press 2 (bases 1 to 770)
             AB032249 770 bp mRNA ROD 13-OCT-2000 Mus musculus masc mRNA for apoptosis-associated speck-like protein containing CARD, complete cds.
                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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Pred. No. 1.1e-16;
0; Mismatches 84; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="masc"
87. .668
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Best Local Similarity 73.2%;
Matches 229; Conservative C
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                                                                                                                    Mus musculus mRNA.
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/note="concar"
/codoc="PYCARD"
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FSFVPSWHLTCKDSLLGALKEIHPYLVMDLEQS"

171 c 188 g 151 t
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                                                                                                                                        Mus musculus
Bukarvota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                       Variance to 701)

Martinon, F., Hofmann, K. and Tschopp, J.

Direct Submission

Burnet (28-SEP-2000) Institute of Biochemistry, University of Lausanne, Ch des Boveresses 155, Epalinges 1066, Switzerland

Location, Qualifiers

1. 701

1. 701

//strain="FVB/N"
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06-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GACCGCGCTGCCCACCCCAGAGCCATGGGGCGGGCGCACGAGATGCCATCCTGGACGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.1%; Score 175.6; DB 94; Length 701; 73.8%; Pred. No. 3e-16; Live 0; Mismatches 79; Indels 0;
    ROD
                                                                                                                                                                          1 (bases 1 to 701)
Martinon,F., Hofmann,K. and Tschopp,J.
Pycard a PYD and CARD containing molecule
10104 701 bp mRNA musculus PYCARD mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/tissue_type="mammary tumor"
/dev_stage="3 month virgin"
27..608
                                                                     AF310104.1 GI:11096300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                 house mouse
    AF310104
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Waterston, R.
Direct Submitssion
Submitted (24-AUG-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 53108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTICE: This sequence represents the full insert of this CDNA. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The separately.
                                                                                                                                                                                                              Woesner, J., Tan, F., Marra, M., Kucaba, T., Yandell, M., Martin, J., Marth, G., Bowles, L., Wylie, T., Bowers, Y., Steptoe, M., Theising, B., Gelsel, S., Allen, M., Underwood, K., Chamberla, J., Person, B., Gibbons, M., Harvey, N., Pape, D., Chamberlain, A., Morales, R., Schurk, R., Ritter, E., Kohn, S., Swaller, T., Behymer, K., Hillier, L., Wilson, R. and Waterston, R.
                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tcccgcgggggcgctgctgtccatggacgccttggacctcaccgacaagctggtcagct 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                   29-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.9%; Score 174.4; DB 97; Length 556; 77.6%; Pred. No. 4.9e-16; Live 0; Mismatches 61; Indels 0;
HUMZD54H05 556 bp mRNA PRI 2
Homo sapiens full length insert cDNA clone ZD54H05.
AF086332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone_llb="Soares_fetal_heart_NbHH19W"
/clone="IMAGE:344505"
168 c 177 g 87 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The location of this clone is unknown Location/Qualifiers
1. 556
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:est@watson.wustl.edu
                                                                              AF086332.1 GI:3483677
                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 556)
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Matches 211; Conservative
                                                                                                                                          Homo sapiens
                                                                                                FLI_CDNA.
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ACCESSION
VERSION
KEYWORDS
SOURCE
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ORIGIN
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AUTHORS
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AUTHORS
TITLE
JOURNAL
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                   Locus
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241 CCTACTACGAGGACTACGCAGCCGAGCTCGTGGCGGCGTGCTGCGCGCACATGCGCATGT 300
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<sup>392</sup> aggagatggccgggcagctgcaggcggccacg 423

Search completed: August 30, 2001, 22:30:38 Job time: 6521 sec

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